

**REMARKS**

Applicants request approval of the revision to Figure 3A correcting the nucleotide at position 152 from "I" to "A". This correction is supported in the nucleotide sequence of SEQ ID NO:5 at 152. The error in Figure 3A is of a typographical nature and does not present new matter.

Applicants have added into the present specification a paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages 1-4. Furthermore, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

The following statement is provided to meet the requirements of 37 C.F.R. §1.821(f) and 1.821(g).

I hereby state, in accordance with 37 C.F.R. §1.821(f), that the content of the attached paper and computer readable copies of the sequence listing are believed to be the same.

I hereby also state, in accordance with 37 C.F.R. §1.821(g), that the submission is not believed to include new matter.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence

and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

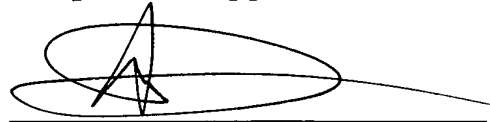
Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

BROWDY AND NEIMARK, P.L.L.C.  
Attorneys for Applicant(s)

By

A handwritten signature in black ink, appearing to be 'Allen C. Yun', is written over a horizontal line. The signature is stylized with a large loop and a trailing flourish.

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FIG. 3A

N3'VH (J1)

FB

## SEQUENCE LISTING

<110> WILLNER, Itamar  
ESHAR, Zelig

<120> DETECTION OF SMALL MOLECULES BY USE OF A PIEZOELECTRIC SENSOR

<130> WILLNER=5

<140> US 09/889,936

<141> 2001-07-25

<150> PCT/IL00/00048

<151> 2000-01-25

<150> IL 128212

<151> 1999-01-25

<160> 8

<170> PatentIn version 3.1

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37

<210> 2

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<212> DNA

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<210> 3

<211> 17

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 ctg tct gat gtg cag ctt cag gag tcg gga cct ggc ctg gtg aag cct 96  
 Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro  
 20 25 30  
 tcc cag tct ctg tcc ctc acc tgc tct gtc act ggt tac tca atc acc 144  
 Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr  
 35 40 45  
 agt ggt tat gcc tgg aac tgg atc cgg cag ttt cca gga aac aaa ctg 192  
 Ser Gly Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu  
 50 55 60  
 gag tgg atg ggc tac ata agc tac agt ggt ttc act agc tac aac cca 240  
 Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Phe Thr Ser Tyr Asn Pro  
 65 70 75 80  
 tct ctc aga agt cga atc tct ttc act cga gac aca tcc aag aac cag 288  
 Ser Leu Arg Ser Arg Ile Ser Phe Thr Arg Asp Thr Ser Lys Asn Gln  
 85 90 95  
 ttc ttc ctg cag ttg aat tct gtg act tct gag gac aca gcc aca tat 336  
 Phe Phe Leu Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr  
 100 105 110  
 tac tgt gca aga tgg gac tac ggt act acc tac ggg tac ttc gat gtc 384  
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 Trp Gly Gln Gly Thr Thr Val Thr  
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Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr  
35 40 45

Ser Gly Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu  
50 55 60

Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Phe Thr Ser Tyr Asn Pro  
65 70 75 80

Ser Leu Arg Ser Arg Ile Ser Phe Thr Arg Asp Thr Ser Lys Asn Gln  
85 90 95

Phe Phe Leu Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr  
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Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu  
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Leu Asn Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys  
35 40 45

cca gga cag cct cct aaa ctt ttg atc tac ggg gta ttt att agg gat 192  
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Val Phe Ile Arg Asp  
 50 55 60

tct ggg gtc cct gat cgc ttc aca ggc agt gga tct gga acc gat ttc 240  
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe  
 65 70 75 80

act ctt acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat tac 288  
 Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr  
 85 90 95

tgt cag aat gat cat att tat ccg tac acg ttc gga ggg ggg acc aag 336  
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 Leu Glu Ile Lys  
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 35 40 45

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Val Phe Ile Arg Asp  
 50 55 60

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe  
 65 70 75 80

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr  
 85 90 95

Cys Gln Asn Asp His Ile Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys  
 100 105 110

Leu Glu Ile Lys  
 115